SEQUENCE LISTING

<110> Rajgarhia, Vineet
Penttila, Merja
Ruohonen, Laura
Ilmen, Marja
Koivuranta, Kari

<120> Methods and materials for synthesis of organic products

<130> MBHB00-1237-A

<140> 09/992,430
<141> 2001-11-23

<150> 60/252541
<151> 2000-11-22

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<170> PatentIn version 3.1

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gacagagacc tgtctacttg ggtttgccat ctaacttcgt tgaccagatg gtcccagcct 480

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acgcttgcgc ttccagacac gatgtcaagg ctgagaccaa gaagttgatt gacatcactc 660

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<213> Unknown

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<223> kanamycin resistance gene fragment

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gtcagcagca tagggaaaca cggcttttcc taccaaactc aaggaattat caaactctgc 180

aacacttgcg tatgcaggta gcaagggaaa tgtcatactt gaagtcggac agtgagtgta 240

gtcttgagaa attctgaagc cgtattttta ttatcagtga gtcagtcatc aggagatcct 300

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gagggagcca cggttgatga gagctttgtt gtaggtggac cagttggtga ttttgaactt 480

ttgctttgcc acggaacggt ctgcgttgtc gggaagatgc gtgatctgat ccttcaactc 540

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cagtgttaca accaattaac caattctgat tagaaaaact catcgagcat caaatgaaac 660

tgcaatttat tcatatcagg attatcaata ccatattttt gaaaaagccg tttctgtaat 720

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atttctttcc agacttgttc aacaggccag ccattacgct cgtcatcaaa atcactcgca 960

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<210> 21
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gta aaa gtt gtg gta gtg gga gtg gga agt gtt ggg tct gcc aca gcg 96

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Val Lys Val Val Val Val Gly Val Gly Ser Val Gly Ser Ala Thr Ala
            20                  25                  30

tat acg ttg ctt ctc agc ggc atc gtt tcc gag att gtc ctt atc gac      144
Tyr Thr Leu Leu Leu Ser Gly Ile Val Ser Glu Ile Val Leu Ile Asp
        35                  40                  45

gtg aac aaa gac aaa gca gag ggt gaa agc atg gac tta aac cac gca      192
Val Asn Lys Asp Lys Ala Glu Gly Glu Ser Met Asp Leu Asn His Ala
    50                  55                  60

gca cct tca aat aca agg tct cga gcg ggt gat tat cct gac tgc gct      240
Ala Pro Ser Asn Thr Arg Ser Arg Ala Gly Asp Tyr Pro Asp Cys Ala
65                  70                  75                  80

ggc gcg gcc att gtt att gtc aca tgt ggg att aac caa aaa aat gga      288
Gly Ala Ala Ile Val Ile Val Thr Cys Gly Ile Asn Gln Lys Asn Gly
                85                  90                  95

caa aca agg atg gat ctt gct gca aaa aat gcc aac att atg ctg gaa      336
Gln Thr Arg Met Asp Leu Ala Ala Lys Asn Ala Asn Ile Met Leu Glu
            100                 105                 110

atc atc ccc aat gtt gcc aaa tat gct cct gat acc atc ctg ctt att      384
Ile Ile Pro Asn Val Ala Lys Tyr Ala Pro Asp Thr Ile Leu Leu Ile
        115                 120                 125

gcc acg aat cct gtc gat gtt ttg acc tat att agc tat aag gcg tca      432
Ala Thr Asn Pro Val Asp Val Leu Thr Tyr Ile Ser Tyr Lys Ala Ser
    130                 135                 140

ggg ttt cca cta agc aga gtt atc ggc tca ggt aca gtt ctg gat act      480
Gly Phe Pro Leu Ser Arg Val Ile Gly Ser Gly Thr Val Leu Asp Thr
145                 150                 155                 160

gct cgt ttt aaa tac atc ctc gga gag cac ttc aag atc tca tcg gac      528
Ala Arg Phe Lys Tyr Ile Leu Gly Glu His Phe Lys Ile Ser Ser Asp
                165                 170                 175

agc atc gat gcc tgt gta att gga gaa cat ggt gat tcg ggt gtg cct      576
Ser Ile Asp Ala Cys Val Ile Gly Glu His Gly Asp Ser Gly Val Pro
            180                 185                 190

gtc tgg tct ctt acc aac atc gac ggc atg aag ctc cgg gat tac tgc      624
Val Trp Ser Leu Thr Asn Ile Asp Gly Met Lys Leu Arg Asp Tyr Cys
        195                 200                 205

gaa aaa gcc aac cac ata ttt gat cag aat gcg ttc cat aga atc ttt      672
Glu Lys Ala Asn His Ile Phe Asp Gln Asn Ala Phe His Arg Ile Phe
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gag caa acg cga gac gct gct tac gat atc atc aag cgc aaa ggc tat      720
Glu Gln Thr Arg Asp Ala Ala Tyr Asp Ile Ile Lys Arg Lys Gly Tyr
225                 230                 235                 240

act tca tat gga atc gca gcg gga tta ctt cgc ata gta aag gcg att      768
Thr Ser Tyr Gly Ile Ala Ala Gly Leu Leu Arg Ile Val Lys Ala Ile
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tta gag gat aca gga tcc aca ctt aca gtt tca acc gtt ggt gat tat 816
Leu Glu Asp Thr Gly Ser Thr Leu Thr Val Ser Thr Val Gly Asp Tyr
260 265 270

ttt ggg gtt gaa caa att gct ata agc gtc cct acc aaa ctc aat aaa 864
Phe Gly Val Glu Gln Ile Ala Ile Ser Val Pro Thr Lys Leu Asn Lys
275 280 285

agt ggg gct cat caa gtg gct gaa ctt tca ctc gat gag aag gaa ata 912
Ser Gly Ala His Gln Val Ala Glu Leu Ser Leu Asp Glu Lys Glu Ile
290 295 300

gaa ttg atg gaa aaa tca gct agt cag atc aaa tca gtg att gag cat 960
Glu Leu Met Glu Lys Ser Ala Ser Gln Ile Lys Ser Val Ile Glu His
305 310 315 320

ctg gag atc aat 972
Leu Glu Ile Asn

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<213> Kluyveromyces thermotolerans

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Tyr Thr Leu Leu Leu Ser Gly Ile Val Ser Glu Ile Val Leu Ile Asp
35 40 45

Val Asn Lys Asp Lys Ala Glu Gly Glu Ser Met Asp Leu Asn His Ala
50 55 60

Ala Pro Ser Asn Thr Arg Ser Arg Ala Gly Asp Tyr Pro Asp Cys Ala
65 70 75 80

Gly Ala Ala Ile Val Ile Val Thr Cys Gly Ile Asn Gln Lys Asn Gly
85 90 95

Gln Thr Arg Met Asp Leu Ala Ala Lys Asn Ala Asn Ile Met Leu Glu
100 105 110

Ile Ile Pro Asn Val Ala Lys Tyr Ala Pro Asp Thr Ile Leu Leu Ile
115 120 125

Ala Thr Asn Pro Val Asp Val Leu Thr Tyr Ile Ser Tyr Lys Ala Ser
130 135 140

Gly Phe Pro Leu Ser Arg Val Ile Gly Ser Gly Thr Val Leu Asp Thr
145 150 155 160

Ala Arg Phe Lys Tyr Ile Leu Gly Glu His Phe Lys Ile Ser Ser Asp
165 170 175

Ser Ile Asp Ala Cys Val Ile Gly Glu His Gly Asp Ser Gly Val Pro
180 185 190

Val Trp Ser Leu Thr Asn Ile Asp Gly Met Lys Leu Arg Asp Tyr Cys
195 200 205

Glu Lys Ala Asn His Ile Phe Asp Gln Asn Ala Phe His Arg Ile Phe
210 215 220

Glu Gln Thr Arg Asp Ala Ala Tyr Asp Ile Ile Lys Arg Lys Gly Tyr
225 230 235 240

Thr Ser Tyr Gly Ile Ala Ala Gly Leu Leu Arg Ile Val Lys Ala Ile
245 250 255

Leu Glu Asp Thr Gly Ser Thr Leu Thr Val Ser Thr Val Gly Asp Tyr
260 265 270

Phe Gly Val Glu Gln Ile Ala Ile Ser Val Pro Thr Lys Leu Asn Lys
275 280 285

Ser Gly Ala His Gln Val Ala Glu Leu Ser Leu Asp Glu Lys Glu Ile
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<400> 29

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tcc aca aca gct tac acg tta tta ttg agt agt ttg gtt gct gaa gtg      96
Ser Thr Thr Ala Tyr Thr Leu Leu Leu Ser Ser Leu Val Ala Glu Val
            20                  25                  30

gtg ttg ata gat gtc gat aaa aga aag gtc gaa ggc caa ttt atg gat     144
Val Leu Ile Asp Val Asp Lys Arg Lys Val Glu Gly Gln Phe Met Asp
        35                  40                  45

ctg aac cac gcg gct cct tta acg aag gag tca cga ttc agt gct ggg     192
Leu Asn His Ala Ala Pro Leu Thr Lys Glu Ser Arg Phe Ser Ala Gly
    50                  55                  60

gac tat gaa agt tgt gct gat gct gcg gtt gta atc gta acg ggc ggg     240
Asp Tyr Glu Ser Cys Ala Asp Ala Ala Val Val Ile Val Thr Gly Gly
65                  70                  75                  80

gct aat cag aaa cct ggt caa act aga atg gag cta gcc gag agg aac     288
Ala Asn Gln Lys Pro Gly Gln Thr Arg Met Glu Leu Ala Glu Arg Asn
                85                  90                  95

gtt aaa atc atg cag gaa gtg atc cct aag att gtg aaa tac gcc ccc     336
Val Lys Ile Met Gln Glu Val Ile Pro Lys Ile Val Lys Tyr Ala Pro
            100                 105                 110

aac gca att ttg ctg att gca aca aac cct gtc gat gta ctt acc tat     384
Asn Ala Ile Leu Leu Ile Ala Thr Asn Pro Val Asp Val Leu Thr Tyr
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        115                 120                 125

gct agt ttg aaa gcg tcg gga ttc cca gca agc cgg gtt att ggt tct      432
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    130                 135                 140

ggg aca gtt ctc gac tct gct cgt ata cag cac aac ctg agc aag cta      480
Gly Thr Val Leu Asp Ser Ala Arg Ile Gln His Asn Leu Ser Lys Leu
145                 150                 155                 160

ttc aat gtt tca tct gaa agt gtc aac gcg ttt att atc ggg gaa cat      528
Phe Asn Val Ser Ser Glu Ser Val Asn Ala Phe Ile Ile Gly Glu His
                165                 170                 175

ggt gac tca agt gtg ccc gtc tgg tcg ctt gct gag att gcc ggc atg      576
Gly Asp Ser Ser Val Pro Val Trp Ser Leu Ala Glu Ile Ala Gly Met
            180                 185                 190

aaa gtg gag gat tac tgt agg cag tcc aag aga aag ttt gac ccc agc      624
Lys Val Glu Asp Tyr Cys Arg Gln Ser Lys Arg Lys Phe Asp Pro Ser
        195                 200                 205

att ctg acc aaa ata tat gag gag tcg cgt gac gcg gca gcc tac atc      672
Ile Leu Thr Lys Ile Tyr Glu Glu Ser Arg Asp Ala Ala Ala Tyr Ile
    210                 215                 220

ata gaa cgc aaa ggc tat acc aat ttc ggg att gca gca ggt ttg gct      720
Ile Glu Arg Lys Gly Tyr Thr Asn Phe Gly Ile Ala Ala Gly Leu Ala
225                 230                 235                 240

agg ata gtg aga gct att ctg aga gat gaa ggt gcc cta tta act gtg      768
Arg Ile Val Arg Ala Ile Leu Arg Asp Glu Gly Ala Leu Leu Thr Val
                245                 250                 255

tct act gta ggt gag cac ttt ggc atg aaa gat gtt tca ttg agt gtt      816
Ser Thr Val Gly Glu His Phe Gly Met Lys Asp Val Ser Leu Ser Val
            260                 265                 270

cca act agg gta gac agg agc ggc gct cac cat gtc gtc gac ctt ctg      864
Pro Thr Arg Val Asp Arg Ser Gly Ala His His Val Val Asp Leu Leu
        275                 280                 285

cta aac gac aag gag ctg gag caa att aaa aca tct gga gcc aag ata      912
Leu Asn Asp Lys Glu Leu Glu Gln Ile Lys Thr Ser Gly Ala Lys Ile
    290                 295                 300

aag tca gcc tgt gat gaa ctt ggc att                                  939
Lys Ser Ala Cys Asp Glu Leu Gly Ile
305                 310
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<210> 30
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<213> Torulaspora pretoriensis

<400> 30

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35 40 45

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50 55 60

Asp Tyr Glu Ser Cys Ala Asp Ala Ala Val Val Ile Val Thr Gly Gly
65 70 75 80

Ala Asn Gln Lys Pro Gly Gln Thr Arg Met Glu Leu Ala Glu Arg Asn
85 90 95

Val Lys Ile Met Gln Glu Val Ile Pro Lys Ile Val Lys Tyr Ala Pro
100 105 110

Asn Ala Ile Leu Leu Ile Ala Thr Asn Pro Val Asp Val Leu Thr Tyr
115 120 125

Ala Ser Leu Lys Ala Ser Gly Phe Pro Ala Ser Arg Val Ile Gly Ser
130 135 140

Gly Thr Val Leu Asp Ser Ala Arg Ile Gln His Asn Leu Ser Lys Leu
145 150 155 160

Phe Asn Val Ser Ser Glu Ser Val Asn Ala Phe Ile Ile Gly Glu His
165 170 175

Gly Asp Ser Ser Val Pro Val Trp Ser Leu Ala Glu Ile Ala Gly Met
180 185 190

Lys Val Glu Asp Tyr Cys Arg Gln Ser Lys Arg Lys Phe Asp Pro Ser
195 200 205

Ile Leu Thr Lys Ile Tyr Glu Glu Ser Arg Asp Ala Ala Ala Tyr Ile
210 215 220

Ile Glu Arg Lys Gly Tyr Thr Asn Phe Gly Ile Ala Ala Gly Leu Ala
225 230 235 240

Arg Ile Val Arg Ala Ile Leu Arg Asp Glu Gly Ala Leu Leu Thr Val
245 250 255

Ser Thr Val Gly Glu His Phe Gly Met Lys Asp Val Ser Leu Ser Val
260 265 270

Pro Thr Arg Val Asp Arg Ser Gly Ala His His Val Val Asp Leu Leu
275 280 285

Leu Asn Asp Lys Glu Leu Glu Gln Ile Lys Thr Ser Gly Ala Lys Ile
290 295 300

Lys Ser Ala Cys Asp Glu Leu Gly Ile
305 310

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<400> 32
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<210> 33
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<400> 33
gctctagatg aaaacacaat ttacacc 27

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<400> 34

atggatcctt acacaaaagc tctgtcgc 28

<210> 35
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<400> 35
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<210> 36
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<400> 36
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<210> 37
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<400> 37
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<210> 38
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<210> 42
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<400> 42
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<210> 43
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tgcacaatag gcatttgcaa gaattactcg tgagtaagga aagagtgagg aactatcgca 180

tacctgcatt taaagatgcc gatttgggcg cgaatccttt attttggctt caccctcata 240

ctattatcag ggccagaaaa aggaagtgtt tccctccttc ttgaattgat gttaccctca 300

taaagcacgt ggcctcttat cgagaaagaa attaccgtcg ctcgtgattt gtttgcaaaa 360

agaacaaaac tgaaaaaacc cagacacgct cgacttcctg tcttcctatt gattgcagct 420

tccaatttcg tcacacaaca aggtcctagc gacggctcac aggttttgta acaagcaatc 480

gaaggttctg gaatggcggg aaagggttta gtaccacatg ctatgatgcc cactgtgatc 540

tccagagcaa agttcgttcg atcgtactgt tactctctct ctttcaaaca gaattgtccg 600

aatcgtgtga caacaacagc ctgttctcac acactctttt cttctaacca agggggtggt 660

ttagtttagt agaacctcgt gaaacttaca tttacatata tataaacttg cataaattgg 720

tcaatgcaag aaatacatat ttggtctttt ctaattcgta gtttttcaag ttcttagatg 780

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gccaaatatg ctcctgatac catcctgctt attgccacga atcctgtcga tgttttgacc 1260

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caatccagag aactggaaag attgtgtagc cttgaaaaac ggtgaaactt acgggtccaa 1920

gattgtctac agattttcct gatttgccag cttactatcc ttcttgaaaa tatgcactct 1980

atatctttta gttcttaatt gcaacacata gatttgctgt ataacgaatt ttatgctatt 2040

ttttaaattt ggagttcagt gataaaagtg tcacagcgaa tttcctcaca tgtagggacc 2100

gaattgttta caagttctct gtaccaccat ggagacatca aaaattgaaa atctatggaa 2160

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<210> 46
<211> 37
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<400> 46
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<400> 47
acttggccat ggtgatagtt attcttctgc aattga 36

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<210> 51

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<222> (21)..(21)
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<220>
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Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser
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<210> 59
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attattag 68

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<400> 62
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<210> 63
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<212> DNA
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ttttgttttt gtttg 75

<210> 64
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<212> DNA
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<400> 64
gcgatctcga gaaagaaacg acccatccaa gtgatg 36

<210> 65
<211> 35
<212> DNA
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<400> 65
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